



SEQUENCE LISTING

<110> GROZINGER, CHRISTINA M.
HASSIG, CHRISTIAN A.
SCHREIBER, STUART L.

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Pro	Leu	Pro	Gly	Pro	Tyr	Asp	Ser	Arg	Asp	Asp	Phe	Pro	Leu	Arg	Lys	245	250	255
Thr	Ala	Ser	Glu	Pro	Asn	Leu	Lys	Val	Arg	Ser	Arg	Leu	Lys	Gln	Lys	260	265	270
Val	Ala	Glu	Arg	Arg	Ser	Ser	Pro	Leu	Leu	Arg	Arg	Lys	Asp	Gly	Thr	275	280	285
Val	Ile	Ser	Thr	Phe	Lys	Lys	Arg	Ala	Val	Glu	Ile	Thr	Gly	Ala	Gly	290	295	300
Pro	Gly	Ala	Ser	Ser	Val	Cys	Asn	Ser	Ala	Pro	Gly	Ser	Gly	Pro	Ser	305	310	315
Ser	Pro	Asn	Ser	Ser	His	Ser	Thr	Ile	Ala	Glu	Asn	Gly	Phe	Thr	Gly	325	330	335
Ser	Val	Pro	Asn	Ile	Pro	Thr	Glu	Met	Leu	Pro	Gln	His	Arg	Ala	Leu	340	345	350
Pro	Leu	Asp	Ser	Ser	Pro	Asn	Gln	Phe	Ser	Leu	Tyr	Thr	Ser	Pro	Ser	355	360	365
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Leu	Leu	Leu	Glu	Gln	Ala	Arg	Gln	Gln	Ser	Thr	Leu	Ile	Ala	Val	Pro	450	455	460
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Met	Arg	Thr	Val	Gly	Lys	Leu	Pro	Arg	His	Arg	Pro	Leu	Ser	Arg	Thr	485	490	495
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Pro	Thr	Thr	His	Pro	Glu	Glu	Thr	Glu	Glu	Glu	Leu	Thr	Glu	Gln	Gln	545	550	555
Glu	Val	Leu	Leu	Gly	Glu	Gly	Ala	Leu	Thr	Met	Pro	Arg	Glu	Gly	Ser	565	570	575
Thr	Glu	Ser	Glu	Ser	Thr	Gln	Glu	Asp	Leu	Glu	Glu	Glu	Asp	Glu	Glu	580	585	590
Glu	Asp	Gly	Glu	Glu	Glu	Glu	Asp	Cys	Ile	Gln	Val	Lys	Asp	Glu	Glu	595	600	605
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Pro	Phe	Trp	Glu	Val	Leu	Val	Arg	Ser	Thr	Glu	Thr	Val	Glu	Arg	Asp	435	440	445
Asn	Met	Glu	Glu	Asp	Asn	Val	Glu	Glu	Ser	Glu	Glu	Glu	Gly	Pro	Trp	450	455	460

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<213> Homo sapiens

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gagtttcatc agtacagttg gtggacgtta attgtttgaa tttgatagtc tttgaattta 3960
atcaagaaac tacctggaac cagtgaagaa gaaagctgga cttaaataat cttagaatta 4020
attgataaat gtctctttta aaatctactg tatttattat aatttacacc cttgaaggtg 4080
atctcttggt ttgtgttgta aatatattgt ttgtatgttt cccttcttgc cttctgttat 4140
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<210> 14
<211> 590
<212> PRT
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<400> 14
Met His Ser Met Ile Ser Ser Val Asp Val Lys Ser Glu Val Pro Val
  1              5              10              15

Gly Leu Glu Pro Ile Ser Pro Leu Asp Leu Arg Thr Asp Leu Arg Met
      20              25              30

Met Met Pro Val Val Asp Pro Val Val Arg Glu Lys Gln Leu Gln Gln
      35              40              45

Glu Leu Leu Leu Ile Gln Gln Gln Gln Gln Ile Gln Lys Gln Leu Leu
      50              55              60

Ile Ala Glu Phe Gln Lys Gln His Glu Asn Leu Thr Arg Gln His Gln
      65              70              75              80

Ala Gln Leu Gln Glu His Ile Lys Glu Leu Leu Ala Ile Lys Gln Gln
      85              90              95

Gln Glu Leu Leu Glu Lys Glu Gln Lys Leu Glu Gln Gln Arg Gln Glu
      100             105             110

Gln Glu Val Glu Arg His Arg Arg Glu Gln Gln Leu Pro Pro Leu Arg
      115             120             125

Gly Lys Asp Arg Gly Arg Glu Arg Ala Val Ala Ser Thr Glu Val Lys
      130             135             140

Gln Lys Leu Gln Glu Phe Leu Leu Ser Lys Ser Ala Thr Lys Asp Thr
      145             150             155             160

Pro Thr Asn Gly Lys Asn His Ser Val Ser Arg His Pro Lys Leu Trp
      165             170             175

Tyr Thr Ala Ala His His Thr Ser Leu Asp Gln Ser Ser Pro Pro Leu
      180             185             190

Ser Gly Thr Ser Pro Ser Tyr Lys Tyr Thr Leu Pro Gly Ala Gln Asp
      195             200             205

Ala Lys Asp Asp Phe Pro Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu
      210             215             220

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Lys	Val	Arg	Ser	Arg	Leu	Lys	Gln	Lys	Val	Ala	Glu	Arg	Arg	Ser	Ser	225	230	235	240
Pro	Leu	Leu	Arg	Arg	Lys	Asp	Gly	Asn	Val	Val	Thr	Ser	Phe	Lys	Lys	245	250	255	
Arg	Met	Phe	Glu	Val	Thr	Glu	Ser	Ser	Val	Ser	Ser	Ser	Ser	Pro	Gly	260	265	270	
Ser	Gly	Pro	Ser	Ser	Pro	Asn	Asn	Gly	Pro	Thr	Gly	Ser	Val	Thr	Glu	275	280	285	
Asn	Glu	Thr	Ser	Val	Leu	Pro	Pro	Thr	Pro	His	Ala	Glu	Gln	Met	Val	290	295	300	
Ser	Gln	Gln	Arg	Ile	Leu	Ile	His	Glu	Asp	Ser	Met	Asn	Leu	Leu	Ser	305	310	315	320
Leu	Tyr	Thr	Ser	Pro	Ser	Leu	Pro	Asn	Ile	Thr	Leu	Gly	Leu	Pro	Ala	325	330	335	
Val	Pro	Ser	Gln	Leu	Asn	Ala	Ser	Asn	Ser	Leu	Lys	Glu	Lys	Gln	Lys	340	345	350	
Cys	Glu	Thr	Gln	Thr	Leu	Arg	Gln	Gly	Val	Pro	Leu	Pro	Gly	Gln	Tyr	355	360	365	
Gly	Gly	Ser	Ile	Pro	Ala	Ser	Ser	Ser	His	Pro	His	Val	Thr	Leu	Glu	370	375	380	
Gly	Lys	Pro	Pro	Asn	Ser	Ser	His	Gln	Ala	Leu	Leu	Gln	His	Leu	Leu	385	390	395	400
Leu	Lys	Glu	Gln	Met	Arg	Gln	Gln	Lys	Leu	Leu	Val	Ala	Gly	Gly	Val	405	410	415	
Pro	Leu	His	Pro	Gln	Ser	Pro	Leu	Ala	Thr	Lys	Glu	Arg	Ile	Ser	Pro	420	425	430	
Gly	Ile	Arg	Gly	Thr	His	Lys	Leu	Pro	Arg	His	Arg	Pro	Leu	Asn	Arg	435	440	445	
Thr	Gln	Ser	Ala	Pro	Leu	Pro	Gln	Ser	Thr	Leu	Ala	Gln	Leu	Val	Ile	450	455	460	
Gln	Gln	Gln	His	Gln	Gln	Phe	Leu	Glu	Lys	Gln	Lys	Gln	Tyr	Gln	Gln	465	470	475	480
Gln	Ile	His	Met	Asn	Lys	Leu	Leu	Ser	Lys	Ser	Ile	Glu	Gln	Leu	Lys	485	490	495	
Gln	Pro	Gly	Ser	His	Leu	Glu	Glu	Ala	Glu	Glu	Glu	Leu	Gln	Gly	Asp	500	505	510	
Gln	Ala	Met	Gln	Glu	Asp	Arg	Ala	Pro	Ser	Ser	Gly	Asn	Ser	Thr	Arg	515	520	525	

Ser Asp Ser Ser Ala Cys Val Asp Asp Thr Leu Gly Gln Val Gly Ala
530 535 540

Val Lys Val Lys Glu Glu Pro Val Asp Ser Asp Glu Asp Ala Gln Ile
545 550 555 560

Gln Glu Met Glu Ser Gly Glu Gln Ala Ala Phe Met Gln Gln Val Ile
565 570 575

Gly Lys Asp Leu Ala Pro Gly Phe Val Ile Lys Val Ile Ile
580 585 590

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<211> 69

<212> PRT

<213> Homo sapiens

<400> 15

His His Ala Lys Lys Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp
1 5 10 15

Ile Val Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu
20 25 30

Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly Val Glu Glu Ala Phe
35 40 45

Tyr Thr Thr Asp Arg Val Met Thr Val Ser Phe His Lys Tyr Gly Glu
50 55 60

Tyr Phe Pro Gly Thr
65

<210> 16

<211> 75

<212> PRT

<213> Saccharomyces sp.

<400> 16

His His Ala Glu Pro Gln Ala Ala Gly Gly Phe Cys Leu Phe Ser Asn
1 5 10 15

Val Ala Val Ala Ala Lys Asn Ile Leu Lys Asn Tyr Pro Glu Ser Val
20 25 30

Arg Arg Ile Met Ile Leu Asp Trp Asp Ile His His Gly Asn Gly Thr
35 40 45

Gln Lys Ser Phe Tyr Gln Asp Asp Gln Val Leu Tyr Val Ser Leu His
50 55 60

Arg Phe Glu Met Gly Lys Tyr Tyr Pro Gly Thr
65 70 75

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<220>
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<223> Any amino acid

<220>
<221> MOD_RES
<222> (6)
<223> Any amino acid

<400> 17
Asn Xaa Xaa Gly Gly Xaa His His Ala
1 5

<210> 18
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
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<400> 18
Arg Pro Pro Gly His His Ala
1 5

<210> 19
<211> 7
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<213> Artificial Sequence

<220>
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<222> (3)
<223> Phe or Tyr

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<223> Any amino acid

<400> 19
Ser Gly Xaa Cys Xaa Xaa Asn
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<213> Artificial Sequence

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<220>
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<222> (2)
<223> Hydrophobic amino acid

<220>
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<223> Hydrophobic amino acid

<220>
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<223> Gln or Glu

<400> 20
Asp Xaa Asp Xaa His His Gly Asp Gly Val Xaa
1 5 10

<210> 21
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<213> Artificial Sequence

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<223> Any amino acid

<400> 21
Asp Xaa Asp Xaa His His Gly Xaa Gly Thr Gln
1 5 10

<210> 22
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<223> Any amino acid

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<223> Any amino acid

<400> 22
Val Xaa Thr Xaa Ser His
1 5

<210> 23
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<223> Met or Leu

<220>
<221> MOD_RES
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<222> (12)

<223> Ser or Thr

<400> 23

Asn Xaa Pro Xaa Xaa Asp Gly Ile Asp Asp Xaa Xaa Tyr
1 5 10

<210> 24

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<212> PRT

<213> Artificial Sequence

<220>

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<400> 24

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1 5

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<210> 26

<211> 6

<212> PRT

<213> Homo sapiens

<400> 26

Gly Gly Tyr Glu Asn Pro

1

5

<210> 27
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<400> 27
Gly Glu Asp Cys Pro
1 5

<210> 28
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<400> 28
Gly Glu Asp Cys Pro
1 5

<210> 29
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<400> 29
Gly Asp Asp Cys Pro
1 5

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Gly Tyr Asp Cys Pro
1 5

<210> 31
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Gly Val Asp Ser Asp Thr
1 5

<210> 32
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<400> 32
Gly Val Asp Ser Asp Thr
1 5

<210> 33
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<400> 33
Gly Val Asp Thr Asp Thr
1 5

<210> 34
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<400> 34
Glu Tyr Ala Phe Pro
1 5

<210> 35
<211> 4
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<400> 35
Glu Tyr Phe Pro
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<210> 36
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<400> 36
Glu Tyr Phe Pro
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<211> 5
<212> PRT
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<400> 37
Asn Tyr Phe Phe Pro
1 5

<210> 38

<211> 5
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<400> 38
Pro Gly Phe Phe Pro
1 5

<210> 39
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<400> 39
Asp Gly Trp Phe Phe Pro
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<210> 40
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Asn Gly Trp Phe Phe Pro
1 5

<210> 41
<211> 6
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<400> 41
Gln Gly Arg Phe Trp Pro
1 5

<210> 42
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<400> 42
His Gly Thr Phe Phe Pro
1 5

<210> 43
<211> 6
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<400> 43
Asp Gly Asn Phe Phe Pro
1 5

<210> 44
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<400> 44
Pro Ala Gly Gly Met His His Ala
1 5

<210> 45
<211> 8
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<400> 45
Trp Ala Gly Gly Leu His His Ala
1 5

<210> 46
<211> 8
<212> PRT
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<400> 46
Trp Ala Gly Gly Leu His His Ala
1 5

<210> 47
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<400> 47
Trp Ala Gly Gly Leu His His Ala
1 5

<210> 48
<211> 8
<212> PRT
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<400> 48
Trp Ser Gly Gly Trp His His Ala
1 5

<210> 49
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<400> 49

Arg Pro Pro Gly His His Ala
1 5

<210> 50

<211> 7

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<213> Homo sapiens

<400> 50

Arg Pro Pro Gly His His Ala
1 5

<210> 51

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Arg Pro Pro Gly His His Ala
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Arg Pro Pro Gly His His Ala
1 5

<210> 53

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<400> 53

Arg Pro Pro Gly His His Ala
1 5

<210> 54

<211> 10

<212> PRT

<213> Homo sapiens

<400> 54

Tyr Ile Asp Leu Asp Ala His His Cys Asp
1 5 10

<210> 55

<211> 10

<212> PRT
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<400> 55
Tyr Ile Asp Ile Asp Ile His His Gly Asp
1 5 10

<210> 56
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<400> 56
Tyr Ile Asp Ile Asp Ile His His Gly Asp
1 5 10

<210> 57
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<400> 57
Tyr Ile Asp Ile Asp Ile His His Gly Asp
1 5 10

<210> 58
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<400> 58
Tyr Val Asp Leu Asp Leu His His Gly Asp
1 5 10

<210> 59
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<400> 59
Ile Val Asp Trp Asp Val His His Gly Asn
1 5 10

<210> 60
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<400> 60
Ile Val Asp Trp Asp Ile His His Gly Asn
1 5 10

<210> 61
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<400> 61
Ile Val Asp Trp Asp Val His His Gly Gln
1 5 10

<210> 62
<211> 10
<212> PRT
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<400> 62
Ile Val Asp Trp Asp Val His His Gly Asn
1 5 10

<210> 63
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<400> 63
Ile Val Asp Trp Asp Val His His Gly Asn
1 5 10

<210> 64
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<400> 64
Gly Gly Gly Tyr
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<210> 65
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Gly Gly Gly Tyr
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<210> 66
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Gly Gly Gly Tyr
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Gly Gly Gly Tyr
1

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Glu Gly Gly His
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<210> 70
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Glu Gly Gly His
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<210> 71
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Glu Gly Gly Tyr
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<210> 72
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Glu Gly Gly Tyr
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<210> 73

<211> 4

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<213> Homo sapiens

<400> 73

Glu Gly Gly His
1

<210> 74

<211> 74

<212> PRT

<213> Homo sapiens

<400> 74

His His Ala Glu Gln Asp Ala Ala Cys Gly Phe Cys Phe Phe Asn
1 5 10 15

Ser Val Ala Val Ala Ala Arg His Ala Gln Thr Ile Ser Gly His Ala
20 25 30

Leu Arg Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr
35 40 45

Gln His Met Phe Glu Asp Asp Pro Ser Val Leu Tyr Val Ser Leu His
50 55 60

Arg Tyr Asp His Gly Thr Phe Phe Pro Met Gly
65 70

<210> 75

<211> 5

<212> PRT

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<220>

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<222> (2)

<223> Cys or Thr

<220>

<221> MOD_RES

<222> (4)

<223> Val or Ile

<400> 75

Asp Xaa Pro Xaa Phe
1 5

<210> 76

<211> 6

<212> PRT

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<220>

<223> Description of Artificial Sequence: Consensus
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<221> MOD_RES

<222> (2)

<223> Phe or Tyr

<220>

<221> MOD_RES

<222> (4)..(5)

<223> Any amino acid

<400> 76

Gly Xaa Cys Xaa Xaa Asn
1 5

<210> 77

<211> 6

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Consensus
sequence

<220>

<221> MOD_RES

<222> (2)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (3)

<223> Val or Phe

<220>

<221> MOD_RES

<222> (5)

<223> Any amino acid

<400> 77

Val Xaa Thr Ser Xaa His
1 5

<210> 78
<211> 5
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<222> (5)
<223> Tyr or His

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Xaa Glu Gly Gly Xaa
1 5